An Anaerobic Methane Oxidizing Community Dominated by ANME-1 in a Non-Hydrate-Associated Gulf of Mexico Sediment

Karen G. Lloyd
Department of Marine Sciences
University of North Carolina – Chapel Hill
12-7 Venable Hall, CB#3300, Chapel Hill, NC 27599
USA
klloyd@email.unc.edu

Laura Lapham
Department of Marine Sciences
University of North Carolina – Chapel Hill
12-7 Venable Hall, CB#3300, Chapel Hill, NC 27599
USA

Andreas Teske
Department of Marine Sciences
University of North Carolina – Chapel Hill
12-7 Venable Hall, CB#3300, Chapel Hill, NC 27599
USA

Anaerobic methane oxidizers, together with methanogens, comprise a methane cycle suitable for oxidant-poor, early earth-like environments. Currently, anaerobic oxidation of methane (AOM) is known to involve the ANME-1 and ANME-2 archaeal phylotypes, which often form consortia with sulfate reducing bacteria. We investigated sediments from site NR1, Gulf of Mexico, using clone libraries of 16S rDNA, *mcrA*, and *dsrAB*; the latter two genes encode enzymes specific for methanogens/ANMEs and sulfate reducers, respectively. The _^{13}C of methane increases towards the sediment-water interface, suggesting that biological methanotrophy contributes to the observed vertical profile of methane disappearance. At a depth of 15-21cm, the archaeal 16S rDNA and *mcrA* clone libraries are dominated by ANME-1. Sequences from the ANME-2 phylotype were not amplified, even though the general archaeal primers used (A8f-A1492r and A21f-A915r) are known to amplify ANME-2; and a primer targeting ANME-2 (EelMS932) was also used. The *mcrA* clone library contains sequences only from ANME-1 and *Methanosarcinales*. The bacterial 16S rDNA and *dsrAB* libraries are much more diverse than the archaeal 16S rDNA and *mcrA* libraries, and they contain only a few sequences that group with putative AOM syntrophs. These sediments appear to harbor a diverse community of sulfate reducing bacteria that are not entirely supported by AOM. The dominance of ANME-1, and absence of ANME-2, may be due to the relatively low methane concentrations (<250μM) of these sediments, which may allow ANME-1 to out-compete ANME-2. These results suggest that ANME-1 is solely responsible for AOM in these marine sediments.